STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 131977

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Friday, September 17, 2004
Case Serial Number: 10/019595

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

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STIC-Biotech/ChemLib 13/977 mg

From: Schultz, James
Sent: Wednesday, September 08, 2004 1:49 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/019,595

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?
Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed: 9/17
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 14:56:58 ; Search time 19497 Seconds
(without alignments)
11639.951 Million cell updates/sec

Title: US-10-019-595-1
Perfect score: 5236
Sequence: 1 cgagcgcggcgcccttgagc.....gtacccggatcctcgaattc 5236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1237800

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
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11: gb_sts:*
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13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		24.4	0.5	29	6	AR162080	AR162080 Sequence
2		24.4	0.5	29	6	AR166605	AR166605 Sequence
3		24.4	0.5	29	6	BD238387	BD238387 Sorting o
4		24.4	0.5	29	6	AR279813	AR279813 Sequence
5		24.4	0.5	29	6	AR288232	AR288232 Sequence
6	c	24.4	0.5	29	6	AX048408	AX048408 Sequence
7		24.4	0.5	29	6	AX048409	AX048409 Sequence
8		24.4	0.5	29	6	AX052994	AX052994 Sequence
9		24.4	0.5	29	6	AX353685	AX353685 Sequence
10		24.4	0.5	29	6	AX662302	AX662302 Sequence
11		24.4	0.5	29	6	BD204968	BD204968 Protein a
12		24.2	0.5	30	6	AR051244	AR051244 Sequence
13		24.2	0.5	30	6	AR127791	AR127791 Sequence
14		24.2	0.5	30	6	I28373	I28373 Sequence 12
15	c	24	0.5	24	6	AR009472	AR009472 Sequence
16	c	24	0.5	24	6	E12007	E12007 Linker. 9/1
17	c	23.8	0.5	28	6	BD234335	BD234335 Improved
18		23.8	0.5	29	6	AX430216	AX430216 Sequence
19		23.8	0.5	29	6	BD165919	BD165919 Method fo
20	c	23.4	0.4	26	6	I79496	I79496 Sequence 3
21	c	23.4	0.4	26	6	BD192375	BD192375 Reagents
22		23.4	0.4	29	6	AX052989	AX052989 Sequence
23	c	23	0.4	25	6	BD234336	BD234336 Improved
24	c	22.8	0.4	26	6	AR174581	AR174581 Sequence
25	c	22.8	0.4	26	6	BD248974	BD248974 Novel cyt
26	c	22.8	0.4	26	6	I79494	I79494 Sequence 1
27	c	22.8	0.4	26	6	AR263648	AR263648 Sequence
28	c	22.8	0.4	26	6	AR374073	AR374073 Sequence
29	c	22.8	0.4	26	6	AX106717	AX106717 Sequence
30		22.8	0.4	30	6	AX079108	AX079108 Sequence
31	c	22.6	0.4	26	6	BD237566	BD237566 Genes and
32	c	22.6	0.4	26	6	AR257336	AR257336 Sequence
33	c	22.6	0.4	26	6	AR263647	AR263647 Sequence
34	c	22.6	0.4	26	6	AX814950	AX814950 Sequence
35	c	22.6	0.4	26	6	BD062456	BD062456 A human 2
36	c	22.6	0.4	27	6	AX327980	AX327980 Sequence
37	c	22.6	0.4	27	6	AX513052	AX513052 Sequence
38	c	22.6	0.4	27	6	AX711956	AX711956 Sequence
39		22.6	0.4	29	6	AR268128	AR268128 Sequence
40		22.4	0.4	24	6	AR010037	AR010037 Sequence
41		22.4	0.4	24	6	AR034772	AR034772 Sequence
42		22.4	0.4	24	6	AR068465	AR068465 Sequence
43		22.4	0.4	24	6	AR105984	AR105984 Sequence
44		22.4	0.4	24	6	AR107972	AR107972 Sequence
45	c	22.4	0.4	24	6	BD234330	BD234330 Improved

ALIGNMENTS

RESULT 1
AR162080
LOCUS AR162080 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6258558.
ACCESSION AR162080
VERSION AR162080.1 GI:16229144
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Method for selection of proteins using RNA-protein fusions
JOURNAL Patent: US 6258558-A 8 10-JUL-2001;
FEATURES Location/Qualifiers

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ORIGIN

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  Best Local Similarity   96.2%;  Pred. No. 2.2e+06;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 2
AR166605
LOCUS       AR166605                  29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6281344.
ACCESSION   AR166605
VERSION     AR166605.1  GI:16241997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 8 28-AUG-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match              0.5%;  Score 24.4;  DB 6;  Length 29;
  Best Local Similarity   96.2%;  Pred. No. 2.2e+06;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 3
BD238387
LOCUS       BD238387                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238387
VERSION     BD238387.1  GI:33048157
KEYWORDS    JP 2002536025-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 5 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/5
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US     09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 4
AR279813
LOCUS       AR279813                  29 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518018.
ACCESSION   AR279813
VERSION     AR279813.1  GI:29714958
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 8 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .29
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ORIGIN

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  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 5
AR288232
LOCUS       AR288232                  29 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6537749.
ACCESSION   AR288232
VERSION     AR288232.1  GI:31675516
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Addressable protein arrays
  JOURNAL   Patent: US 6537749-A 3 25-MAR-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 6
AX048408/c
LOCUS       AX048408                  29 bp    DNA     linear   PAT 12-JAN-2001
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DEFINITION  Sequence 7 from Patent WO0071747.
ACCESSION   AX048408
VERSION     AX048408.1  GI:12225572
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 7 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db         26 AAAAAAAAAAAAAAAAAAAAAAAACC 1


RESULT 7
AX048409
LOCUS       AX048409                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 8 from Patent WO0071747.
ACCESSION   AX048409
VERSION     AX048409.1  GI:12225573
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 8 30-NOV-2000;
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FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   96.2%;  Pred. No. 2.2e+06;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
                || ||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 8
AX052994
LOCUS       AX052994                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 10 from Patent WO0071749.
ACCESSION   AX052994
VERSION     AX052994.1  GI:12227096
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 10 30-NOV-2000;
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 9
AX353685
LOCUS       AX353685                  29 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 5 from Patent WO0204656.
ACCESSION   AX353685
VERSION     AX353685.1  GI:18618749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wagner,P. and Polakowski,T.
  TITLE     Bio-probes and use thereof
  JOURNAL   Patent: WO 0204656-A 5 17-JAN-2002;
            Xzillion GmbH & CO.KG (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 10
AX662302
LOCUS       AX662302                  29 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 41 from Patent WO02059293.
ACCESSION   AX662302
VERSION     AX662302.1  GI:29163186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Forster,A.C. and Blacklow,S.C.
  TITLE     Process and compositions for peptide, protein and peptidomimetic
            synthesis
  JOURNAL   Patent: WO 02059293-A 41 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
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Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 11
BD204968
LOCUS       BD204968                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein array enabling site specification.
ACCESSION   BD204968
VERSION     BD204968.1  GI:33014738
KEYWORDS    JP 2002510505-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Protein array enabling site specification
  JOURNAL   Patent: JP 2002510505-A 3 09-APR-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002510505-A/3
            PD   09-APR-2002
            PF   31-MAR-1999 JP 2000542484
            PR   03-APR-1998 US    60/080686
            PI   ROBERT G KUIMELIS,RICHARD WAGNER
            PC   C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
              G01N33/68,
            PC   C12N15/00
            CC   Oligonucleotide used for attaching puromycin
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 12
AR051244
LOCUS       AR051244                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5830658.
ACCESSION   AR051244
VERSION     AR051244.1  GI:5974608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
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  JOURNAL   Patent: US 5830658-A 12 03-NOV-1998;
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Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
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Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 13
AR127791
LOCUS       AR127791                  30 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 12 from patent US 6180777.
ACCESSION   AR127791
VERSION     AR127791.1  GI:14114386
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Horn,T.
  TITLE     Synthesis of branched nucleic acids
  JOURNAL   Patent: US 6180777-A 12 30-JAN-2001;
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Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
              | | ||| ||||||||||||||||||||||||||||
Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 14
I28373
LOCUS       I28373                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 12 from patent US 5571677.
ACCESSION   I28373
VERSION     I28373.1  GI:1819149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 12 05-NOV-1996;
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Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
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Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 15
AR009472/c
LOCUS       AR009472                  24 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 22 from patent US 5756295.
ACCESSION   AR009472
VERSION     AR009472.1  GI:3968277
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Onda,H. and Hosoya,M.
  TITLE     DNA primer and a method for screening DNAS
  JOURNAL   Patent: US 5756295-A 22 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5212 CCATGGTACCCGGATCCTCGAATT 5235
                ||||||||||||||||||||||||
Db         24 CCATGGTACCCGGATCCTCGAATT 1


Search completed: September 15, 2004, 22:19:07
Job time : 19500 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 13:12:42 ; Search time 1798 Seconds
(without alignments)
12371.282 Million cell updates/sec

Title: US-10-019-595-1
Perfect score: 5236
Sequence: 1 cgagcgcggcgcccttgagc.....gtacccggatcctcgaattc 5236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 2723956

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		24.4	0.5	29	3	AAA94315	Aaa94315 RNA-prote
2		24.4	0.5	29	4	AAS00066	Aas00066 Synthetic
3		24.4	0.5	29	4	AAH20990	Aah20990 C-myc epi
4		24.4	0.5	29	6	AAK98637	Aak98637 S cerevis
5		24.4	0.5	30	2	AAV48087	Aav48087 Oligonucl
6		24.2	0.5	30	2	AAQ83940	Aaq83940 Oligonucl
7		24.2	0.5	30	5	AAF60462	Aaf60462 Oligonucl
8	c	24	0.5	24	2	AAQ50581	Aaq50581 Asparagin
9	c	23.8	0.5	28	3	AAA40358	Aaa40358 pBluescri
10		23.8	0.5	29	6	ABN83378	Abn83378 Mononucle
11	c	23.4	0.4	25	2	AAX84258	Aax84258 PCR prime
12	c	23.4	0.4	26	2	AAX07466	Aax07466 Human BS1
13	c	23.4	0.4	26	2	AAX78723	Aax78723 Human pan
14	c	23.4	0.4	27	2	AAV71936	Aav71936 Anchored
15		23.2	0.4	29	4	AAF74918	Aaf74918 CD40L pol
16		23.2	0.4	29	4	AAF74907	Aaf74907 CD40L pol
17		23.2	0.4	29	4	AAF74935	Aaf74935 CD40L pol
18		23.2	0.4	29	4	AAF74921	Aaf74921 CD40L pol
19		23.2	0.4	29	4	AAF74928	Aaf74928 CD40L pol
20		23.2	0.4	30	4	AAF74908	Aaf74908 CD40L pol
21	c	22.8	0.4	26	4	AAD03682	Aad03682 Human ful
22	c	22.8	0.4	26	6	AAS20596	Aas20596 Human zsi
23	c	22.8	0.4	26	6	ABS52638	Abs52638 Human sec
24	c	22.8	0.4	26	6	AAD45055	Aad45055 ZC7764a p
25	c	22.8	0.4	26	6	AAS20671	Aas20671 Human zal
26	c	22.8	0.4	26	7	ABX93599	Abx93599 Human zsi
27	c	22.8	0.4	27	2	AAV71935	Aav71935 Anchored
28		22.8	0.4	30	4	AAF26221	Aaf26221 APC bindi
29	c	22.6	0.4	26	6	AAS20595	Aas20595 Human zsi
30	c	22.6	0.4	26	6	ABS52637	Abs52637 Human sec
31	c	22.6	0.4	26	6	AAD45054	Aad45054 ZC7231 pr
32	c	22.6	0.4	26	7	AAD55692	Aad55692 Bovine vi
33	c	22.6	0.4	26	7	ABX93598	Abx93598 Human zsi
34	c	22.6	0.4	26	9	ACF36382	Acf36382 Nucleotid
35	c	22.6	0.4	27	6	ABQ76254	Abq76254 Murine SC
36	c	22.6	0.4	27	7	ABX12469	Abx12469 Coxsackie
37		22.6	0.4	29	2	AAQ68614	Aaq68614 tRNAPolyU
38		22.6	0.4	29	2	AAT09934	Aat09934 Reverse t
39	c	22.4	0.4	24	2	AAT01340	Aat01340 Tomato ac
40		22.4	0.4	24	2	AAT99286	Aat99286 POLYA, a
41		22.4	0.4	24	2	AAV31743	Aav31743 Nucleotid
42		22.4	0.4	24	2	AAX04086	Aax04086 Oligonucl
43	c	22.4	0.4	24	3	AAA40359	Aaa40359 pBluescri
44	c	22.4	0.4	24	3	AAA40353	Aaa40353 pBluescri
45	c	22.4	0.4	24	4	AAF99756	Aaf99756 Immunosti

ALIGNMENTS

RESULT 1
AAA94315
ID AAA94315 standard; DNA; 29 BP.
XX
AC AAA94315;
XX
DT 11-JAN-2001 (first entry)
XX
DE RNA-protein fusion oligonucleotide 30-P.
XX
KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 29
FT /*tag= a
FT /mod_base= OTHER
FT /note= "attached to puromycin, a peptide acceptor"
XX
PN WO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 43; 121pp; English.
XX
CC The present sequence is one of a number of oligonucleotides which were
CC used for the generation of RNA-protein fusions, including fusions having
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC and in vitro or in situ translation of an mRNA molecule with a peptide

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CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 24.4;  DB 3;  Length 29;
  Best Local Similarity  96.2%;  Pred. No. 8.6e+04;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 2
AAS00066
ID   AAS00066 standard; DNA; 29 BP.
XX
AC   AAS00066;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Synthetic branched encoding molecule sequence.
XX
KW   Addressing element; microarray; protein display;
KW   branched encoding molecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   9. .10
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "AXA, where X is a branching monomer, linked to
FT                   nucleotide 16 of sequence in AAS00065 via a (Hexaethylene
FT                   oxide)n linkage"
FT   modified_base   30
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Other= Covalently linked to puromycin"
XX
PN   WO200116352-A1.
XX
PD   08-MAR-2001.
XX
PF   25-AUG-2000; 2000WO-US023414.
XX
PR   27-AUG-1999;   99US-0151261P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kuimelis RG;
XX
DR   WPI; 2001-183261/18.
XX
PT   Encoding and sorting in vitro translated proteins, useful for the
PT   identification of desired binding partners, comprises attaching a nucleic
PT   acid linker to the protein and binding an encoding molecule to the
PT   linker.
XX
PS   Example 3; Fig 9B; 48pp; English
XX
CC   The sequence represents part of a branched encoding molecule used in
CC   methods to hybridise a capture probe to the addressing element of a DNA
CC   linker attached to an in vitro translated protein, in order to immobilise
CC   the protein to a solid support. The new methods are useful for tagging or
CC   encoding in vitro translated proteins with unique and minimal encoding
CC   molecules and sorting these molecules onto solid supports. They are also
CC   useful for the identification of a desired binding partner. The method
CC   allows the use of pre-made sets of universal encoding molecules, such as
CC   nucleic acid(s) (analogues). These can be used in conjunction with
CC   corresponding universal microarrays or sets of microparticles to create
CC   new protein display systems which are flexible, modular, scalable and
CC   cost effective. The method allows the use of nucleic acid analogue which
CC   are not susceptible to enzymatic incorporation or polymerisation and are
CC   superior to conventional DNA/RNA. The proteins can also be labelled with
CC   fluorescent groups which can be used to monitor the protein in real time.
CC   The absence of RNA is advantageous as they can adopt secondary structures
CC   which are difficult to predict and can interfere with hybridisation steps
CC   and protein folding/function
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 24.4;  DB 4;  Length 29;
  Best Local Similarity  96.2%;  Pred. No. 8.6e+04;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 3
AAH20990
ID   AAH20990 standard; DNA; 29 BP.
XX
AC   AAH20990;
XX
DT   31-AUG-2001  (first entry)
XX
DE   C-myc epitope puromycin linker primer #1.
XX
KW   C-myc; epitope; detection; amplification; biomedical diagnosis;
KW   environmental monitoring; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200142494-A2.
XX
PD   14-JUN-2001.
XX
PF   20-OCT-2000; 2000WO-EP010336.
XX
PR   10-DEC-1999;   99DE-01059857.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Burgstaller P,  Konz D;
XX
DR   WPI; 2001-381706/40.
XX
PT   System for detecting immobilized analyte, useful e.g. for biomedical
PT   diagnosis, has as detection agent specific polypeptide coupled to nucleic
PT   acid for signal amplification.
XX
PS   Example; Page 6; 12pp; German.
XX
CC   This invention describes a novel test system (A) which comprises at least
CC   one immobilized analyte (I) on an insoluble carrier and a polypeptide
CC   detection agent (II), specific for (I) and conjugated, via a linker, to
CC   an amplifier (III). (A) is used for direct, in vitro detection of (I)
CC   with amplification of the signal by polymerase chain reaction (PCR), or a
CC   related technique, applied to (III). The method is useful in biomedical
CC   diagnosis and environmental monitoring and can be used to detect
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CC   range of (I), e.g. diagnostic or pharmaceutical agents, secondary
CC   metabolites, herbicides or pesticides. (A) allow simultaneous, parallel
CC   detection of many different analytes (high throughput capacity),
CC   relatively simply (only a few incubation and washing steps are required)
CC   and with high sensitivity and selectivity. This sequence represents
CC   primer used in the ampification of the c-myc DNA fragment which encodes
CC   an epitope used to illustrate the method of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 24.4;  DB 4;  Length 29;
  Best Local Similarity   96.2%;  Pred. No. 8.6e+04;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || ||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 4
AAK98637
ID   AAK98637 standard; DNA; 29 BP.
XX
AC   AAK98637;
XX
DT   19-APR-2002  (first entry)
XX
DE   S cerevisiae alpha factor receptor STE2 vector linker.
XX
KW   Biological material detection; electrophoresis; bioprobe isolation;
KW   alpha factor receptor; STE2; linker; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "modified by puromycin"
XX
PN   WO200204656-A2.
XX
PD   17-JAN-2002.
XX
PF   26-JUN-2001; 2001WO-EP007259.
XX
PR   07-JUL-2000; 2000DE-01033194.
XX
PA   (XZIL-) XZILLION GMBH & CO KG.
XX
PI   Wagner P,  Polakowski T;
XX
DR   WPI; 2002-154934/20.
XX
PT   Detecting and purifying biological material by (di)electrophoresis,
PT   useful e.g. for separating tissues and viruses, comprises using a probe
PT   that alters (di)electrophoretic properties.
XX
PS   Example 1; Page 12; 20pp; German.
XX
CC   The present invention relates to a method for the detection or
CC   purification of biological material by electrophoresis, which comprises
CC   (i) treating the biological material containing different species with a
CC   bioprobe and (ii) establishing an electric field for detection or
CC   purification of at least one complex formed between the biological
CC   material being tested and a specifically bound bioprobe. The method is
CC   used for detection and purification of tissue, cells, cell organelles,
CC   viruses, proteins, nucleic acids, lipids and/or other organic compounds.
CC   It can also be used for the isolation of specific bioprobes from a
CC   library of bioprobes. The present sequence is a linker described in the
CC   exemplification of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 24.4;  DB 6;  Length 29;
  Best Local Similarity   96.2%;  Pred. No. 8.6e+04;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || ||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29


RESULT 5
AAV48087
ID   AAV48087 standard; DNA; 30 BP.
XX
AC   AAV48087;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 30-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   30
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 24.4;  DB 2;  Length 30;
  Best Local Similarity   96.2%;  Pred. No. 8.8e+04;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
```

```
Db          4 AAAAAAAAAAAAAAAAAAAAAAAAAACC 29
```

RESULT 6
AAQ83940
ID AAQ83940 standard; DNA; 30 BP.
XX
AC AAQ83940;
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
DE Oligonucleotide clamp o, for producing comb-type brached polymer.
XX
KW HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT modified_base   1
FT   /*tag= a
FT   /note= "Modified with SP(O-)(=O)-"
XX
PN WO9501365-A1.
XX
PD 12-JAN-1995.
XX
PF 05-JUL-1994;   94WO-US007557.
XX
PR 02-JUL-1993;   93US-00087386.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Gryaznov SM;
XX
DR WPI; 1995-060944/08.
XX
PT Synthesis of branched polymers and novel branched polymeric structures -
PT used as molecular probes esp. for detecting poly-nucleotide(s).
XX
PS Example 8; Page 33; 52pp; English.
XX
CC The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
CC construction of an oligonucleotide clamp. The clamp is a comb-type
CC branched polymer which has 3' termini and was used to bind a target
CC sequence comprising a segment of the HIV pol and nef genes in single
CC stranded or double stranded forms. An oligonucleotide clamp is a compound
CC capable of forming a covalently closed macromolecule or a stable circular
CC complex after specifically binding to the target polynucleotide.
CC Oligonucleotide clamps generally comprise one or more oligonucleotide
CC moieties capable of specific binding to the target molecule and one or
CC more pairs of binding moieties covalently linked to the oligonucleotide
CC moieties. Upon annealing of the oligonucleotides moieties to the target
CC polynucleotide, the binding moieties of a pair are bought into
CC juxtaposition so that they form a stable covalent or non-covalent linkage
CC or complex. The interaction of the binding moieties effectively clamps
CC the specifically annealed oligonucleotide moieties to the target
CC polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 24.2;  DB 2;  Length 30;
  Best Local Similarity   89.7%;  Pred. No. 9.7e+04;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
                 | | ||| ||||||||||||||||||||||||
Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAAA 29
```

RESULT 7
AAF60462
ID AAF60462 standard; DNA; 30 BP.
XX
AC AAF60462;
XX
DT 27-APR-2001 (first entry)
XX
DE Oligonucleotide clamp #22.
XX
KW Oligonucleotide clamp; ds.
XX
OS Unidentified.
XX
PN US6180777-B1.
XX
PD 30-JAN-2001.
XX
PF 03-JAN-1997;   97US-00787321.
XX
PR 12-JAN-1996;   96US-0009918P.
XX
PA (FARB) BAYER CORP.
XX
PI Horn T;
XX
DR WPI; 2001-201911/20.
XX
PT Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
PS Example 8; Col 19; 20pp; English.
XX
CC The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the
CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention
XX
SQ Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 24.2;  DB 5;  Length 30;
  Best Local Similarity   89.7%;  Pred. No. 9.7e+04;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
                 | | ||| ||||||||||||||||||||||||
Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAAA 29
```

RESULT 8
AAQ50581/c
ID AAQ50581 standard; DNA; 24 BP.
XX
AC AAQ50581;
XX
DT 25-MAR-2003 (revised)
DT 24-MAY-1994 (first entry)
XX
DE Asparaginylendopeptidase oligonucleotide.
XX
KW Asparaginylendopeptidase; Canavalia ensiformis; seed; L-asparagine;
KW primer; PCR; protein fragmentation; peptide synthesis; ss.
XX
OS Synthetic.
XX
PN JP05276960-A.
XX
PD 26-OCT-1993.

```
XX
PF   07-AUG-1992;   92JP-00231602.
XX
PR   07-FEB-1992;   92JP-00056023.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1993-373587/47.
XX
PT   New gene for encoding asparaginyl endo-peptidase - comprises 8 specified
PT   DNA sequences.
XX
PS   Disclosure; Page 29; 35pp; Japanese.
XX
CC   A gene encoding asparaginylendopeptidase is claimed. 8 DNA sequences are
CC   given (AAQ50559-66). The enzyme is a protease derived from a seed of
CC   Canavalia ensiformis which selectively hydrolyses C-terminus amide bond
CC   of L-asparagine residue (see AAR43033 and AAR43041). THe enzyme is useful
CC   for protein fragmentation and enzymatic peptide synthesis. The primers
CC   given in AAQ50567-68, AAQ50576-77 and AAQ50583-90 were used in the
CC   isolation of the fragments given in AAQ50569-75 and AAQ50578-79, by PCR.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+04;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5212 CCATGGTACCCGGATCCTCGAATT 5235
              ||||||||||||||||||||||||
Db         24 CCATGGTACCCGGATCCTCGAATT 1


RESULT 9
AAA40358/c
ID   AAA40358 standard; DNA; 28 BP.
XX
AC   AAA40358;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 8.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 3; Page 67; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 23.8;  DB 3;  Length 28;
  Best Local Similarity   92.6%;  Pred. No. 1.2e+05;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACCA 5214
              || |||||||||||||||||||||||| |
Db         28 AAAAAAAAAAAAAAAAAAAAAAAACTA 2


RESULT 10
ABN83378
ID   ABN83378 standard; DNA; 29 BP.
XX
AC   ABN83378;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Mononucleotide repeat locus BAT25 probe #1.
XX
KW   Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    29
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Labelled with Fluorescein"
XX
PN   EP1207210-A1.
XX
PD   22-MAY-2002.
XX
PF   13-NOV-2001; 2001EP-00126930.
XX
PR   15-NOV-2000; 2000EP-00124897.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Dietmaier W;
XX
DR   WPI; 2002-437469/47.
XX
PT   Analyzing repeat sequences in DNA using a probe which hybridizes to
PT   adjacent repetitive and non-repetitive regions and determining hybrid
PT   melting point is useful to detect microsatellite instability such as in
PT   hereditary cancer.
XX
PS   Claim 16; Page 7; 19pp; English.
XX
CC   The present invention relates to a method for analysing a target nucleic
CC   acid consisting of repetitive and non-repetitive sequences. The method
CC   comprises hybridising a polynucleotide probe comprising a segment
CC   complementary to a non-repetitive region and a segment complementary to
CC   an adjacent repetitive region, where the second segment consists of a
CC   defined number of repeats, and determining the melting point temperature
CC   of the hybrid. The method is used to analyse microsatellites, especially
CC   microsatellite instability, particularly as a means for detecting
CC   hereditary tumours. Alternatively, the method is used to identify an
CC   individual in a population. The present sequence is a probe for
```

```
CC   Mononucleotide repeat locus BAT25, and was used to illustrate the
CC   invention
XX
SQ   Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 23.8;  DB 6;  Length 29;
  Best Local Similarity   92.6%;  Pred. No. 1.2e+05;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACCA 5214
              || ||||||||||||||||||||||| ||
Db          3 AAAAAAAAAAAAAAAAAAAAAAAATCA 29


RESULT 11
AAX84258/c
ID   AAX84258 standard; DNA; 25 BP.
XX
AC   AAX84258;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Example 1; Page 76; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 23.4;  DB 2;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.4e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
              ||| ||||||||||||||||||||||||
Db         25 CAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 12
AAX07466/c
ID   AAX07466 standard; cDNA; 26 BP.
XX
AC   AAX07466;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Human BS124 specific EST clone oligonucleotide.
XX
KW   BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9859049-A1.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-US012862.
XX
PR   20-JUN-1997;   97US-00879354.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Billing-Medel PA,  Cohen M,  Colpitts TL,  Friedman PN,  Gordon J;
PI   Granados EN,  Hodges SC,  Klass MR,  Kratochvil JD,  Russell JC;
PI   Scheffel CP,  Stroupe SD,  Yu H;
XX
DR   WPI; 1999-105623/09.
XX
PT   New isolated BS124 polynucleotides and polypeptides - used for detecting,
PT   diagnosing, preventing or treating diseases or conditions of the breast,
PT   such as breast cancer.
XX
PS   Disclosure; Page 97; 125pp; English.
XX
CC   The sequence is that of an oligonucleotide used in the isolation of a
CC   BS124-specific EST clone. It is useful for detecting, diagnosing,
CC   staging, preventing or treating, or determining predisposition to
CC   diseases or conditions of the breast, such as breast cancer
XX
SQ   Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.4%;  Score 23.4;  DB 2;  Length 26;
  Best Local Similarity   96.0%;  Pred. No. 1.4e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
              ||| ||||||||||||||||||||||||
Db         26 CAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 13
AAX78723/c
ID   AAX78723 standard; DNA; 26 BP.
XX
AC   AAX78723;
XX
DT   03-SEP-1999  (first entry)
XX
DE   Human pancreatic PA153 EST-specific clone primer 12.
XX
KW   Pancreatic disease; PA153; human; cytostatic; detection; antigen;
KW   anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
KW   gene therapy; EST; expressed sequence tag; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931274-A2.
XX
PD   24-JUN-1999.
XX
PF   11-DEC-1998;   98WO-US026441.
XX
PR   15-DEC-1997;   97US-00990568.
XX
PA   (ABBO ) ABBOTT LAB.
XX
```

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
DR WPI; 1999-405041/34.
XX
PT PA153 cDNA transcribed from pancreatic tissue.
XX
PS Example 2; Page 121; 123pp; English.
XX
CC This invention describes novel contiguous and partially overlapping cDNA
CC sequences and their encoded polypeptides, designated PA153, transcribed
CC from human pancreatic tissue and which have cytostatic activity. The
CC PA153 polynucleotides, proteins and antibodies are all useful in methods
CC of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
CC antibodies in a sample is indicative of pancreatic disease. PA153
CC antibodies (antagonists) can also be used in vivo for therapeutic use,
CC e.g. treatment of pancreatic disease, tumours or metastases. Antisense
CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
CC AAX78712-X78725 represent primers used in the method of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.4; DB 2; Length 26;
Best Local Similarity 96.0%; Pred. No. 1.4e+05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAA 5211
||| ||||||||||||||||||||||
Db 26 CAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 14
AAV71936/c
ID AAV71936 standard; DNA; 27 BP.
XX
AC AAV71936;
XX
DT 18-FEB-1999 (first entry)
XX
DE Anchored poly T RT-PCR primer.
XX
KW Normalised; cDNA library; mRNA cloning; reverse transcription;
KW immobilise; screening; hybridisation; nucleic acid amplification;
KW expression pattern; drug development; PCR primer; RT-PCR; ss.
XX
OS Synthetic.
XX
PN WO9851789-A2.
XX
PD 19-NOV-1998.
XX
PF 13-MAY-1998; 98WO-DK000186.
XX
PR 13-MAY-1997; 97DK-00000547.
PR 19-MAY-1997; 97US-00871030.
PR 27-MAR-1998; 98DK-00000432.
XX
PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
PI Warthoe PR;
XX
DR WPI; 1999-009772/01.
XX
PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT reverse transcription and amplification, used to screen for new genes and
PT interacting proteins, potential drugs, and for diagnosis.
XX
PS Example 1; Page 29; 71pp; English.
XX
CC The invention relates to preparation of a normalised, subdivided library
CC of amplified cDNA from the coding regions of mRNA in a sample. The method
CC involves reverse transcription, with at least one cDNA primer of formula
CC 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
CC of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4
CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
CC cDNA synthesis using the first strand as template and a second cDNA
CC primer of a similar formula, in the presence of DNA polymerase I (or its
CC Klenow fragment) and amplification of double-stranded cDNA with a set of
CC amplification primers. Comparison of cDNA in the prepared library with a
CC database (a computer-generated list of molecular weights of restricted
CC DNA fragments of known sequence) is used to determine presence of an
CC expressed protein in a cell, also to detect changes in such expression
CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
CC cDNA stably immobilised on it, obtained by a similar method, are used to
CC screen for genes of a particular family, by hybridisation with nucleic
CC acid from the family (to identify new genes) and to detect differences in
CC expression patterns between cells. The polypeptides expressed by the
CC libraries can be used for drug development. Sequences AAV71935 to
CC AAV71946 represent primers used to exemplify the method of the invention
XX
SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.4; DB 2; Length 27;
Best Local Similarity 96.0%; Pred. No. 1.4e+05;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
||| ||||||||||||||||||||||
Db 26 CAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 15
AAF74918
ID AAF74918 standard; DNA; 29 BP.
XX
AC AAF74918;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:15.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.2; DB 4; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.6e+05;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACCAT 5215
              || |||||||||||||| |||||||| |
Db          1 AAAAAAAAAAAAAAAAACAAAAAACCTT 28
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Search completed: September 15, 2004, 16:54:03
Job time : 1802 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:11:08 ; Search time 323 Seconds
(without alignments)
8996.046 Million cell updates/sec

Title: US-10-019-595-1
Perfect score: 5236
Sequence: 1 cgagcgcggcgcccttgagc.....gtacccggatcctcgaattc 5236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 628400

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24.4	0.5	29	3	US-09-244-794A-8	Sequence 8, Appli
	2	24.4	0.5	29	3	US-09-007-005-8	Sequence 8, Appli
	3	24.4	0.5	29	3	US-09-247-190-8	Sequence 8, Appli
	4	24.4	0.5	29	3	US-09-244-796-8	Sequence 8, Appli
	5	24.4	0.5	29	4	US-09-238-710-8	Sequence 8, Appli
	6	24.4	0.5	29	4	US-09-282-734-3	Sequence 3, Appli
	7	24.2	0.5	30	1	US-08-455-627-12	Sequence 12, Appl
	8	24.2	0.5	30	2	US-08-689-856-12	Sequence 12, Appl
	9	24.2	0.5	30	3	US-08-787-321-12	Sequence 12, Appl
c	10	24	0.5	24	1	US-08-566-037A-22	Sequence 22, Appl
	11	23.8	0.5	29	4	US-10-003-998A-7	Sequence 7, Appli
c	12	23.4	0.4	26	1	US-08-621-914A-3	Sequence 3, Appli
	13	23.4	0.4	30	4	US-09-648-040-4	Sequence 4, Appli
c	14	22.8	0.4	26	1	US-08-621-914A-1	Sequence 1, Appli
c	15	22.8	0.4	26	4	US-09-522-217-38	Sequence 38, Appl
c	16	22.8	0.4	26	4	US-09-527-345-7	Sequence 7, Appli
c	17	22.8	0.4	26	4	US-09-923-246-38	Sequence 38, Appl
c	18	22.8	0.4	26	4	US-10-295-723-38	Sequence 38, Appl
c	19	22.6	0.4	26	4	US-09-527-345-6	Sequence 6, Appli
c	20	22.6	0.4	26	4	US-09-167-513-10	Sequence 10, Appl
c	21	22.6	0.4	26	4	US-09-161-939A-43	Sequence 43, Appl
	22	22.6	0.4	29	4	US-08-227-476-5	Sequence 5, Appli
	23	22.4	0.4	24	1	US-08-014-943A-25	Sequence 25, Appl
	24	22.4	0.4	24	1	US-08-486-421-50	Sequence 50, Appl
	25	22.4	0.4	24	1	US-08-470-911-50	Sequence 50, Appl
	26	22.4	0.4	24	2	US-08-735-381-1	Sequence 1, Appli
	27	22.4	0.4	24	2	US-08-486-809-50	Sequence 50, Appl
	28	22.4	0.4	24	3	US-09-183-619-7	Sequence 7, Appli
	29	22.4	0.4	24	3	US-09-201-674-1	Sequence 1, Appli
	30	22.4	0.4	24	4	US-09-536-936-11	Sequence 11, Appl
	31	22.4	0.4	24	4	US-09-025-639-4	Sequence 4, Appli
	32	22.4	0.4	24	4	US-09-333-237-4	Sequence 4, Appli
	33	22.4	0.4	24	4	US-09-732-067-1	Sequence 1, Appli
	34	22.4	0.4	24	4	US-10-043-415-4	Sequence 4, Appli
	35	22.4	0.4	24	4	US-09-854-317-1	Sequence 1, Appli
c	36	22.4	0.4	24	4	US-09-721-154-1	Sequence 1, Appli
c	37	22.4	0.4	25	1	US-08-341-148-2	Sequence 2, Appli
c	38	22.4	0.4	25	1	US-08-460-130-2	Sequence 2, Appli
c	39	22.4	0.4	25	3	US-08-969-813-1	Sequence 1, Appli
c	40	22.4	0.4	25	3	US-09-183-619-5	Sequence 5, Appli
c	41	22.4	0.4	25	4	US-09-282-734-23	Sequence 23, Appl
c	42	22.4	0.4	25	5	PCT-US94-14096-2	Sequence 2, Appli
c	43	22.4	0.4	26	1	US-08-621-914A-2	Sequence 2, Appli
c	44	22.4	0.4	26	3	US-08-873-437-2	Sequence 2, Appli
c	45	22.4	0.4	26	3	US-09-197-951-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-244-794A-8
; Sequence 8, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-794A-8

Query Match 0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || ||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
```

RESULT 2
US-09-007-005-8
; Sequence 8, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B

; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-8

Query Match 0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
|| ||||||||||||||||||||||||||
Db 4 AAAAAAAAAAAAAAAAAAAAAAAACC 29

RESULT 3
US-09-247-190-8
; Sequence 8, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/247,190
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-21
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-8

Query Match 0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
|| ||||||||||||||||||||||||||
Db 4 AAAAAAAAAAAAAAAAAAAAAAAACC 29

RESULT 4
US-09-244-796-8
; Sequence 8, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-8

Query Match 0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
|| ||||||||||||||||||||||||||
Db 4 AAAAAAAAAAAAAAAAAAAAAAAACC 29

RESULT 5
US-09-238-710-8
; Sequence 8, Application US/09238710A
; Patent No. 6518018
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350004
; CURRENT APPLICATION NUMBER: US/09/238,710A
; CURRENT FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-238-710-8

Query Match 0.5%; Score 24.4; DB 4; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
|| ||||||||||||||||||||||||||
Db 4 AAAAAAAAAAAAAAAAAAAAAAAACC 29

RESULT 6
US-09-282-734-3
; Sequence 3, Application US/09282734A
; Patent No. 6537749
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002

; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin
US-09-282-734-3

Query Match 0.5%; Score 24.4; DB 4; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
```

RESULT 7
US-08-455-627-12
; Sequence 12, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-12

Query Match 0.5%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
              | | ||| ||||||||||||||||||||||
Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAA 29
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RESULT 8
US-08-689-856-12
; Sequence 12, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-12

Query Match 0.5%; Score 24.2; DB 2; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       5183 CTCTCAACAAAAAAAAAAAAAAAAAAAA 5211
              | | ||| ||||||||||||||||||||||
Db          1 CACACAAAAAAAAAAAAAAAAAAAAAAA 29
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RESULT 9
US-08-787-321-12
; Sequence 12, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (l300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: oligonucleotide
US-08-787-321-12

Query Match 0.5%; Score 24.2; DB 3; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5183 CTCTCAACAAAAAAAAAAAAAAAAAAAAAA 5211
| | ||| ||||||||||||||||||||||||||
Db 1 CACACAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 10
US-08-566-037A-22/c
; Sequence 22, Application US/08566037A
; Patent No. 5756295
; GENERAL INFORMATION:
; APPLICANT: Haruo ONDA et al.
; TITLE OF INVENTION: DNA PRIMER AND A METHOD FOR
; TITLE OF INVENTION: SCREENING DNAS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/566,037A
; FILING DATE: December 1, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; MOLECULE TYPE: Synthetic DNA
US-08-566-037A-22

Query Match 0.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5212 CCATGGTACCCGGATCCTCGAATT 5235
||||||||||||||||||||||||
Db 24 CCATGGTACCCGGATCCTCGAATT 1

RESULT 11
US-10-003-998A-7
; Sequence 7, Application US/10003998A
; Patent No. 6664064
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
; TITLE OF INVENTION: products
; FILE REFERENCE: 5438/00/EP
; CURRENT APPLICATION NUMBER: US/10/003,998A
; CURRENT FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-998A-7

Query Match 0.5%; Score 23.8; DB 4; Length 29;
Best Local Similarity 92.6%; Pred. No. 8.4e+03;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACCA 5214
|| |||||||||||||||||||||||| ||
Db 3 AAAAAAAAAAAAAAAAAAAAAAAATCA 29

RESULT 12
US-08-621-914A-3/c
; Sequence 3, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-621-914A-3

Query Match 0.4%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 9.9e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAA 5211
||| ||||||||||||||||||||||
Db 26 CAAAAAAAAAAAAAAAAAAAAAAA 2

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RESULT 13
US-09-648-040-4
; Sequence 4, Application US/09648040
; Patent No. 6436665
; GENERAL INFORMATION:
;  APPLICANT: Robert G. Kuimelis
;  TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
;  TITLE OF INVENTION:  TRANSLATED PROTEINS
;  FILE REFERENCE: 50036/032002
;  CURRENT APPLICATION NUMBER: US/09/648,040
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: US 60/151,261
;  PRIOR FILING DATE: 1999-08-27
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Encoding molecule
;   NAME/KEY: misc_feature
;   LOCATION: 10
;   OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4

  Query Match             0.4%;  Score 23.4;  DB 4;  Length 30;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || || ||||||||||||||||||||||
Db             5 AAAAANAAAAAAAAAAAAAAAAAACC 30


RESULT 14
US-08-621-914A-1/c
; Sequence 1, Application US/08621914A
; Patent No. 5707807
;  GENERAL INFORMATION:
;    APPLICANT:  KATO, KIKUYA
;    TITLE OF INVENTION:  MOLECULAR INDEXING FOR EXPRESSED GENE
;    TITLE OF INVENTION:  ANALYSIS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,914A
;      FILING DATE:  26-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LAWRENCE III, STANTON T.
;      REGISTRATION NUMBER:  25,736
;      REFERENCE/DOCKET NUMBER:  7005-107-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  other nucleic acid
US-08-621-914A-1

  Query Match             0.4%;  Score 22.8;  DB 1;  Length 26;
  Best Local Similarity   92.3%;  Pred. No. 1.4e+04;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5186 TCAACAAAAAAAAAAAAAAAAAAAA 5211
              | || ||||||||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 15
US-09-522-217-38/c
; Sequence 38, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
;  APPLICANT: No. 6307024ak, Julia E.
;  APPLICANT: Presnell, Scott R.
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT: Foster, Donald C.
;  APPLICANT: Holly, Richard D.
;  APPLICANT: Gross, Jane A.
;  APPLICANT: Johnston, Janet V.
;  APPLICANT: Nelson, Andrew J.
;  APPLICANT: Dillon, Stacey R.
;  APPLICANT: Hammond, Angela K.
;  TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;  FILE REFERENCE: 99-16
;  CURRENT APPLICATION NUMBER: US/09/522,217
;  CURRENT FILING DATE: 2000-03-09
;  EARLIER APPLICATION NUMBER: US 60/123,547
;  EARLIER FILING DATE: 1999-03-09
;  EARLIER APPLICATION NUMBER: US 60/123,904
;  EARLIER FILING DATE: 1999-03-11
;  EARLIER APPLICATION NUMBER: US 60/142,013
;  EARLIER FILING DATE: 1999-07-01
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-522-217-38

  Query Match             0.4%;  Score 22.8;  DB 4;  Length 26;
  Best Local Similarity   92.3%;  Pred. No. 1.4e+04;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5186 TCAACAAAAAAAAAAAAAAAAAAAA 5211
              | || ||||||||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAA 1


Search completed: September 16, 2004, 01:46:03
Job time : 325 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:24:03 ; Search time 2188 Seconds
(without alignments)
12040.701 Million cell updates/sec

Title: US-10-019-595-1
Perfect score: 5236
Sequence: 1 cgagcgcggcgcccttgagc.....gtacccggatcctcgaattc 5236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	24.4	0.5	29	9	US-09-282-734-3	Sequence 3, Appli
	2	24.4	0.5	29	10	US-09-876-235-8	Sequence 8, Appli
	3	24.4	0.5	29	15	US-10-348-627-3	Sequence 3, Appli
	4	24.4	0.5	29	17	US-10-057-783A-41	Sequence 41, Appl
c	5	23.4	0.4	26	9	US-09-099-823-14	Sequence 14, Appl
	6	23.4	0.4	30	15	US-10-217-914-4	Sequence 4, Appli
c	7	22.8	0.4	26	9	US-09-922-480-7	Sequence 7, Appli
c	8	22.8	0.4	26	9	US-09-923-236-7	Sequence 7, Appli
c	9	22.8	0.4	26	9	US-09-923-246-38	Sequence 38, Appl
c	10	22.8	0.4	26	9	US-09-922-469-7	Sequence 7, Appli
c	11	22.8	0.4	26	15	US-10-295-723-38	Sequence 38, Appl
c	12	22.8	0.4	26	17	US-10-659-684-38	Sequence 38, Appl
c	13	22.6	0.4	26	9	US-09-922-480-6	Sequence 6, Appli
c	14	22.6	0.4	26	9	US-09-923-236-6	Sequence 6, Appli
c	15	22.6	0.4	26	9	US-09-922-469-6	Sequence 6, Appli
c	16	22.6	0.4	26	15	US-10-039-876A-10	Sequence 10, Appl
c	17	22.6	0.4	26	15	US-10-196-703-43	Sequence 43, Appl
c	18	22.6	0.4	26	15	US-10-352-253A-36	Sequence 36, Appl
c	19	22.6	0.4	26	16	US-10-224-289-20	Sequence 20, Appl
c	20	22.6	0.4	27	13	US-10-071-214-42	Sequence 42, Appl
c	21	22.4	0.4	24	9	US-09-920-342-12	Sequence 12, Appl
c	22	22.4	0.4	24	9	US-09-920-313-148	Sequence 148, App
c	23	22.4	0.4	24	10	US-09-949-305B-6	Sequence 6, Appli
c	24	22.4	0.4	24	10	US-09-888-326-841	Sequence 841, App
c	25	22.4	0.4	24	10	US-09-776-479-433	Sequence 433, App
c	26	22.4	0.4	24	10	US-09-776-479-961	Sequence 961, App
	27	22.4	0.4	24	10	US-09-776-479-962	Sequence 962, App
c	28	22.4	0.4	24	13	US-10-058-270A-140	Sequence 140, App
c	29	22.4	0.4	24	13	US-10-314-578-433	Sequence 433, App
c	30	22.4	0.4	24	13	US-10-314-578-961	Sequence 961, App
	31	22.4	0.4	24	13	US-10-314-578-962	Sequence 962, App
c	32	22.4	0.4	24	13	US-09-776-479-433	Sequence 433, App
c	33	22.4	0.4	24	13	US-09-776-479-961	Sequence 961, App
	34	22.4	0.4	24	13	US-09-776-479-962	Sequence 962, App
c	35	22.4	0.4	24	13	US-10-671-628-10	Sequence 10, Appl
	36	22.4	0.4	24	14	US-10-043-415-4	Sequence 4, Appli
c	37	22.4	0.4	24	15	US-10-112-653-415	Sequence 415, App
c	38	22.4	0.4	24	15	US-10-112-653-919	Sequence 919, App
	39	22.4	0.4	24	15	US-10-112-653-920	Sequence 920, App
c	40	22.4	0.4	24	15	US-10-017-995-433	Sequence 433, App
c	41	22.4	0.4	24	15	US-10-017-995-961	Sequence 961, App
	42	22.4	0.4	24	15	US-10-017-995-962	Sequence 962, App
c	43	22.4	0.4	24	15	US-10-058-513-39	Sequence 39, Appl
c	44	22.4	0.4	24	15	US-10-272-502A-2	Sequence 2, Appli
c	45	22.4	0.4	24	15	US-10-224-523-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-282-734-3
; Sequence 3, Application US/09282734A
; Publication No. US20020182597A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin
US-09-282-734-3

Query Match 0.5%; Score 24.4; DB 9; Length 29;
Best Local Similarity 96.2%; Pred. No. 2.7e+04;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
             || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
```

RESULT 2
US-09-876-235-8
; Sequence 8, Application US/09876235
; Publication No. US20030022236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.

; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/876,235
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-876-235-8

Query Match 0.5%; Score 24.4; DB 10; Length 29;
Best Local Similarity 96.2%; Pred. No. 2.7e+04;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
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RESULT 3
US-10-348-627-3
; Sequence 3, Application US/10348627
; Publication No. US20030143616A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/10/348,627
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US/09/282,734A
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin
US-10-348-627-3

Query Match 0.5%; Score 24.4; DB 15; Length 29;
Best Local Similarity 96.2%; Pred. No. 2.7e+04;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
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RESULT 4
US-10-057-783A-41
; Sequence 41, Application US/10057783A
; Publication No. US20040091955A1
; GENERAL INFORMATION:
; APPLICANT: Forster, Anthony C.
; TITLE OF INVENTION: Process and compositions for peptide, protein and
; TITLE OF INVENTION: peptidomimetic synthesis
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/10/057,783A
; CURRENT FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:FROM SYNTHETIC
; OTHER INFORMATION: DNA
US-10-057-783A-41

Query Match 0.5%; Score 24.4; DB 17; Length 29;
Best Local Similarity 96.2%; Pred. No. 2.7e+04;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          4 AAAAAAAAAAAAAAAAAAAAAAAACC 29
```

RESULT 5
US-09-099-823-14/c
; Sequence 14, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: SCHEFFEL, CHRISTI
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: YU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,823
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,354
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6120.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-823-14

Query Match 0.4%; Score 23.4; DB 9; Length 26;
Best Local Similarity 96.0%; Pred. No. 4.7e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAA 5211
||| ||||||||||||||||||||||
Db 26 CAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 6
US-10-217-914-4
; Sequence 4, Application US/10217914
; Publication No. US20030013160A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; TITLE OF INVENTION: TRANSLATED PROTEINS
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/10/217,914
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 09/648,040
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-10-217-914-4

Query Match 0.4%; Score 23.4; DB 15; Length 30;
Best Local Similarity 92.3%; Pred. No. 5.3e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
|| || ||||||||||||||||||||||||
Db 5 AAAAANAAAAAAAAAAAAAAAAAACC 30

RESULT 7
US-09-922-480-7/c
; Sequence 7, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-922-480-7

Query Match 0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 8
US-09-923-236-7/c
; Sequence 7, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-236-7

Query Match 0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 9
US-09-923-246-38/c
; Sequence 38, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-246-38

Query Match 0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 10
US-09-922-469-7/c
; Sequence 7, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-922-469-7

Query Match 0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
US-10-295-723-38/c
; Sequence 38, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38

Query Match 0.4%; Score 22.8; DB 15; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 12
US-10-659-684-38/c
; Sequence 38, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-659-684-38

Query Match 0.4%; Score 22.8; DB 17; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAAAAAAAAAAAAAAAAA 5211
| || ||||||||||||||||||||||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13
US-09-922-480-6/c
; Sequence 6, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.

; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-480-6

Query Match 0.4%; Score 22.6; DB 9; Length 26;
Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
:|| ||||||||||||||||||||||
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 14
US-09-923-236-6/c
; Sequence 6, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-923-236-6

Query Match 0.4%; Score 22.6; DB 9; Length 26;
Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
:|| ||||||||||||||||||||||
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 15
US-09-922-469-6/c
; Sequence 6, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-469-6

Query Match 0.4%; Score 22.6; DB 9; Length 26;
Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAAAAAAAAAAAAAAAAAA 5211
:|| ||||||||||||||||||||||
Db 26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

Search completed: September 16, 2004, 02:22:36
Job time : 2189 secs

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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:08:59 ; Search time 12080 Seconds
(without alignments)
12943.574 Million cell updates/sec

Title: US-10-019-595-1
Perfect score: 5236
Sequence: 1 cgagcgcggcgcccttgagc.....gtacccggatcctcgaattc 5236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 38748

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	24.4	0.5	28	28	AZ481286	AZ481286 1M0303L24
	2	24.4	0.5	29	14	T67079	T67079 ya52f07.r3
	3	24.4	0.5	29	28	AZ819924	AZ819924 2M0091A19
c	4	24	0.5	30	28	AZ458127	AZ458127 1M0261I24
c	5	23.8	0.5	28	28	AZ809971	AZ809971 2M0074C14
	6	23.8	0.5	29	14	CF328476	CF328476 NACL--03-
c	7	23.4	0.4	25	14	N33150	N33150 yy06g01.s1
c	8	23.4	0.4	26	14	CF296851	CF296851 30DGS--07
	9	23.4	0.4	26	28	AZ485624	AZ485624 1M0313H11
c	10	23.4	0.4	27	14	N52529	N52529 yv35a12.s1
c	11	23.4	0.4	28	9	AL587582	AL587582 AL587582
	12	23.4	0.4	28	14	CF299294	CF299294 7LEAF--03
c	13	23.4	0.4	29	13	BQ590537	BQ590537 E012843-0
c	14	23	0.4	24	14	CA853764	CA853764 B12A03.se
c	15	23	0.4	24	14	CF312319	CF312319 ABF--07-P
c	16	23	0.4	25	29	CG726337	CG726337 1119089E1
c	17	23	0.4	28	14	T52836	T52836 ya81b09.s1
c	18	23	0.4	30	14	CF299716	CF299716 7LEAF--03
	19	22.8	0.4	26	2	HSM003162	Al038686 Homo sapi
	20	22.8	0.4	28	14	CF337400	CF337400 JMT--07-N
c	21	22.8	0.4	28	14	R37697	R37697 yf50c03.s1
c	22	22.8	0.4	29	28	AZ492630	AZ492630 1M0326B22
	23	22.6	0.4	30	12	BG865511	BG865511 602783643
	24	22.6	0.4	30	28	AZ962183	AZ962183 2M0230I24
	25	22.4	0.4	24	12	BG670391	BG670391 DRNBAF06
c	26	22.4	0.4	24	13	BX554611	BX554611 BX554611
	27	22.4	0.4	24	14	CF276855	CF276855 14ETL--02
c	28	22.4	0.4	24	14	CF301561	CF301561 7LEAF--06
c	29	22.4	0.4	24	14	CF320862	CF320862 HD--11-O1
	30	22.4	0.4	24	28	AZ328848	AZ328848 1M0052M17
	31	22.4	0.4	24	28	AZ363562	AZ363562 1M0109G10
	32	22.4	0.4	24	28	AZ386491	AZ386491 1M0145D02
c	33	22.4	0.4	24	28	AZ390642	AZ390642 1M0152H07
	34	22.4	0.4	24	28	AZ404871	AZ404871 1M0173J14
c	35	22.4	0.4	24	28	AZ459280	AZ459280 1M0264A05
c	36	22.4	0.4	24	28	AZ644621	AZ644621 1M0508F12
	37	22.4	0.4	24	28	AZ786257	AZ786257 2M0031H11
	38	22.4	0.4	24	28	AZ834990	AZ834990 2M0129A05
	39	22.4	0.4	24	28	AZ970038	AZ970038 2M0243J02
	40	22.4	0.4	24	28	AZ984490	AZ984490 2M0266H05
c	41	22.4	0.4	24	28	AZ993423	AZ993423 2M0278O19
c	42	22.4	0.4	24	29	TA169D12P	AL478922 T. brucei
	43	22.4	0.4	24	29	TA27B08Q	AL453584 T. brucei
	44	22.4	0.4	24	29	TA354C06P	AL494439 T. brucei
	45	22.4	0.4	24	29	TA371F11P	AL495622 T. brucei

ALIGNMENTS

RESULT 1
AZ481286/c
LOCUS AZ481286 28 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0303L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0303L24 F, genomic survey sequence.
ACCESSION AZ481286
VERSION AZ481286.1 GI:10642351
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0303  row: L  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0303L24"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match              0.5%;  Score 24.4;  DB 28;  Length 28;
  Best Local Similarity   96.2%;  Pred. No. 1.6e+07;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5187 CAACAAAAAAAAAAAAAAAAAAAAC 5212
                ||| ||||||||||||||||||||| ,
Db         28 CAAAAAAAAAAAAAAAAAAAAAAAC 3


RESULT 2
T67079
LOCUS       T67079                   29 bp    mRNA    linear   EST 07-MAR-1995
DEFINITION  ya52f07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:66565 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   T67079
VERSION     T67079.1  GI:676519
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence starts: 1
            High qality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: T7
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:66565"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares fetal liver spleen 1NFLS"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      1st strand cDNA was primed with a Pac I - oligo(dT) primer
                      [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match              0.5%;  Score 24.4;  DB 14;  Length 29;
  Best Local Similarity   92.6%;  Pred. No. 1.6e+07;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5184 TCTCAACAAAAAAAAAAAAAAAAAAAAA 5210
                ||||||| ||||||| ||||||||||||
Db          3 TCTCAAAAAAAAAAANAAAAAAAAAAAA 29


RESULT 3
AZ819924
LOCUS       AZ819924                 29 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0091A19 R, genomic survey sequence.
ACCESSION   AZ819924
VERSION     AZ819924.1  GI:12989832
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0091  row: A  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.5%; Score 24.4; DB 28; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.6e+07;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAACC 5213
              || |||||||||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAAAAAAAAC 28
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RESULT 4
AZ458127/c
LOCUS AZ458127 30 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0261I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261I24 R, genomic survey sequence.
ACCESSION AZ458127
VERSION AZ458127.1 GI:10616252
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: I column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
FEATURES Location/Qualifiers
source 1. .30

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261I24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.5%; Score 24; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAA 5211
              ||||||||||||||||||||||||
Db         25 AACAAAAAAAAAAAAAAAAAAAAA 2
```

RESULT 5
AZ809971/c
LOCUS AZ809971 28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074C14 F, genomic survey sequence.
ACCESSION AZ809971
VERSION AZ809971.1 GI:12976769
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: C column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
source 1. .28

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.5%; Score 23.8; DB 28; Length 28;
Best Local Similarity 92.6%; Pred. No. 2e+07;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5190 CAAAAAAAAAAAAAAAAAAAAAACCATG 5216
||||||||||||||||||||||||| || |
Db 28 CAAAAAAAAAAAAAAAAAAAAAAGCAAG 2

RESULT 6
CF328476
LOCUS CF328476 29 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-G12, mRNA sequence.
ACCESSION CF328476
VERSION CF328476.1 GI:33805199
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-G12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match 0.5%; Score 23.8; DB 14; Length 29;
Best Local Similarity 92.6%; Pred. No. 2e+07;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5188 AACAAAAAAAAAAAAAAAAAAAAACCA 5214
|| |||||||||||||||||||||||| |
Db 1 AAAAAAAAAAAAAAAAAAAAAAAACAA 27

RESULT 7
N33150/c
LOCUS N33150 25 bp mRNA linear EST 10-JAN-1996
DEFINITION yy06g01.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270480 3' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);, mRNA sequence.
ACCESSION N33150
VERSION N33150.1 GI:1153549
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGE:270480"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

```
  Query Match             0.4%;  Score 23.4;  DB 14;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+07;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAAC 5212
              || |||||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAC 1


RESULT 8
CF296851/c
LOCUS       CF296851                 26 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-G13, mRNA sequence.
ACCESSION   CF296851
VERSION     CF296851.1  GI:33665884
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-G13"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match             0.4%;  Score 23.4;  DB 14;  Length 26;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+07;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5188 AACAAAAAAAAAAAAAAAAAAAAAC 5212
              || |||||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAC 1


RESULT 9
AZ485624
LOCUS       AZ485624                 26 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0313H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0313H11 F, genomic survey sequence.
ACCESSION   AZ485624
VERSION     AZ485624.1  GI:10651606
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0313  row: H  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0313H11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.4%;  Score 23.4;  DB 28;  Length 26;
  Best Local Similarity   96.0%;  Pred. No. 2.4e+07;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5191 AAAAAAAAAAAAAAAAAAAACCAT 5215
              |||||||||||||||||||| ||||
Db          1 AAAAAAAAAAAAAAAAAAAATCCAT 25


RESULT 10
N52529/c
LOCUS       N52529                   27 bp    mRNA    linear   EST 15-FEB-1996
DEFINITION  yv35a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
            HIN-1 (HUMAN);, mRNA sequence.
ACCESSION   N52529
VERSION     N52529.1  GI:1193695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
```

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  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: m13 -40 forward
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3793948"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:244702"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             0.4%;  Score 23.4;  DB 14;  Length 27;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+07;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5186 TCAACAAAAAAAAAAAAAAAAAAAA 5211
              || | ||||||||||||||||||||||
Db         26 TCNAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 11
AL587582/c
LOCUS       AL587582                  28 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587582 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS059D03, mRNA sequence.
ACCESSION   AL587582
VERSION     AL587582.1  GI:13192616
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059D03"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"
ORIGIN

  Query Match             0.4%;  Score 23.4;  DB 9;  Length 28;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+07;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5190 CAAAAAAAAAAAAAAAAAAAAACCAT 5215
              ||||||||||||||||||||||  ||
Db         26 CAAAAAAAAAAAAAAAAAAAAANAAT 1


RESULT 12
CF299294
LOCUS       CF299294                  28 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-E04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-E04, mRNA sequence.
ACCESSION   CF299294
VERSION     CF299294.1  GI:33671055
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-E04"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN

  Query Match             0.4%;  Score 23.4;  DB 14;  Length 28;
  Best Local Similarity   96.0%;  Pred. No. 2.3e+07;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       5188 AACAAAAAAAAAAAAAAAAAAAAAC 5212
              || |||||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAC 25


RESULT 13
BQ590537/c
LOCUS       BQ590537                 29 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-C03-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-C03 3-PRIME, mRNA sequence.
ACCESSION   BQ590537
VERSION     BQ590537.1  GI:26120120
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 29   Std Error: 0.00
            Plate: 19  row: C  column: 03
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189579"
                     /db_xref="taxon:161934"
                     /clone="024-019-C03"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match              0.4%;  Score 23.4;  DB 13;  Length 29;
  Best Local Similarity   96.0%;  Pred. No. 2.3e+07;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5187 CAACAAAAAAAAAAAAAAAAAAAA 5211
              ||| ||||||||||||||||||||||
Db         28 CAAAAAAAAAAAAAAAAAAAAAAA 4


RESULT 14
CA853764/c
LOCUS       CA853764                 24 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  B12A03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
            B12A03 5', mRNA sequence.
ACCESSION   CA853764
VERSION     CA853764.1  GI:33390569
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="B12A03"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 12hr SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from roots of soybean cv. Peking 12  hrs after
                     infection by SCN race 3. These are cloned in pBluescript
                     SK- phagemid. "
ORIGIN

  Query Match              0.4%;  Score 23;  DB 14;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+07;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5191 AAAAAAAAAAAAAAAAAAAAAACC 5213
              ||||||||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAAAAACC 1


RESULT 15
CF312319/c
LOCUS       CF312319                 24 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-P12.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-P12, mRNA sequence.
ACCESSION   CF312319
VERSION     CF312319.1  GI:33684080
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
```

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

```
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             0.4%;  Score 23;  DB 14;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+07;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5191 AAAAAAAAAAAAAAAAAAAAACC 5213
             |||||||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAAAACC 1


Search completed: September 16, 2004, 01:40:37
Job time : 12085 secs
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